



The biogeography of methanotrophs: field studies and meta-analysis

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Methane emission from an environment depends not only on production, but also on methane oxidation. The *pmoA* gene encoding a subunit of the methane monooxygenase is a suitable functional and phylogenetic marker gene for the methanotrophic bacteria (MOB) responsible for this process in terrestrial habitats.

On the regional scale, we designed a factorial experiment in the rice growing area around Vercelli (Italy) including three different locations, two rice varieties, and two habitats (soil and roots). Multivariate analysis of fingerprints (T-RFLP) revealed different community patterns at the three sites located 10 to 20 kilometers apart. Root samples were characterized by a high abundance of type I MOB whereas the rice variety had no effect. With the current agronomical practice being nearly identical, historical contingencies might be responsible for the site differences. Considering a large reservoir of viable yet inactive MOB cells acting as a microbial seed bank, past management practice may have shaped the communities.

A meta-analysis of the environmental distribution patterns of *pmoA* genotypes was performed using approximately 3400 high-quality environmental sequences from public databases. It showed a distinct clustering of upland soil sequences and sequences retrieved from halophilic environments, respectively. Furthermore, wetland rice and freshwater sequences dominate different type Ib clusters that are only distantly related to any cultivated MOB. Genotypes specifically correlated with paddy fields showed a wide geographical distribution ranging from Japan through China and the Subcontinent to the Mediterranean.

In summary, the rice field environment selects for particular methanotrophs, but still allows some variation that may be visible even decades after the effect was generated. Linking structure of the community to its performance and controls remains challenging, because characterized isolates represent only poorly the methanotrophic diversity.